

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2002, 04:48:40 ; Search time 63 Seconds

(without alignments)
3261.818 Million cell updates/sec

Title: US-09-784-340-2

Perfect score: 2802

Sequence: 1 MRSDKSAVFLILQLFCVGC.....KCFLESCQKFKTRIKRE 527

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 350425 segs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-TRANS-human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
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Database : Published.Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2797	99.8	1584	9	US-09-962-678-3

5	2797	99.8	3006	9	US-09-962-678-1	Sequence 1, Appl1
6	1721.5	61.4	1889	9	US-09-981-353-83	Sequence 83, Appl1
7	1713	61.1	2090	10	US-09-880-107-3292	Sequence 3292, Ap
8	1691.5	60.4	2130	9	US-09-981-353-45	Sequence 45, Appl1
9	1689	60.3	2093	10	US-09-880-107-3842	Sequence 3842, Ap
10	1685	60.1	1961	10	US-09-917-800A-1403	Sequence 1403, Ap
11	1684	60.1	1713	9	US-09-880-107-3286	Sequence 3286, Ap
12	1676.5	59.8	2124	9	US-09-981-353-193	Sequence 193, Appl
13	1676.5	59.8	1855	10	US-09-880-107-2120	Sequence 2120, Ap
14	1676.5	58.4	2799	10	US-09-880-107-3756	Sequence 3756, Ap
15	1604.5	57.3	1712	9	US-09-981-353-189	Sequence 189, Appl
16	1137	40.6	2349	12	US-09-981-353-151	Sequence 151, Appl
17	1137	40.6	2349	12	US-10-044-090-845	Sequence 845, Appl
18	1093.5	39.0	2320	10	US-09-835-082-3	Sequence 1, Appl1
19	1093.5	39.0	2320	10	US-09-835-082-3	Sequence 1, Appl1
20	1077	38.4	2422	10	US-09-880-107-2106	Sequence 2106, Ap
21	1076.5	38.4	2380	12	US-10-044-090-816	Sequence 816, Appl
22	1076.5	38.4	2385	9	US-09-981-353-153	Sequence 153, Appl
23	821.5	29.3	2448	10	US-09-967-768A-187	Sequence 187, Appl
24	755.5	27.0	735	10	US-09-305-856B-17	Sequence 17, Appl
25	700.5	25.0	2074	10	US-09-822-830A-262	Sequence 262, Appl
26	698.5	24.9	1851	10	US-09-740-029-1	Sequence 1, Appl1
27	697.5	24.9	1572	10	US-09-895-728-3	Sequence 3, Appl1
28	697.5	24.9	2082	10	US-09-895-728-1	Sequence 1, Appl1
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31	597	21.3	601	10	US-09-917-800A-1433	Sequence 1433, Ap
32	573	20.4	419	10	US-09-960-352-9640	Sequence 9640, Ap
33	565	20.2	588	10	US-09-833-381-344	Sequence 344, Appl
34	562	20.1	582	10	US-09-867-701-1453	Sequence 1453, Appl
35	557	19.9	378	10	US-09-960-352-13060	Sequence 13060, Ap
36	554	19.8	426	10	US-09-960-352-13860	Sequence 13860, A
37	502	17.9	416	10	US-09-960-352-12236	Sequence 12236, A
38	486	17.3	370	10	US-09-960-352-3236	Sequence 3236, Ap
39	455	16.2	417	10	US-09-960-352-11024	Sequence 11024, A
40	441	15.7	334	9	US-09-981-353-149	Sequence 149, Appl
41	436	15.6	345	10	US-09-960-352-8015	Sequence 8015, Ap
42	409.5	14.6	381	10	US-09-960-352-2070	Sequence 2070, Ap
43	398	14.2	413	10	US-09-960-352-3208	Sequence 3208, Ap
44	391	14.0	391	10	US-09-738-873-21	Sequence 21, Appl
45	386.5	13.8	350	10	US-09-960-352-2069	Sequence 2069, Ap

ALIGNMENTS

RESULT 1
US-09-981-353-165
Sequence 165, Application US/09981353
Patent No. US20020160382A1
GENERAL INFORMATION:
APPLICANT: Lasek, Amy W.
APPLICANT: Jones, David A.
TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
FILE REFERENCE: PA-0038 US
CURRENT APPLICATION NUMBER: US/09/981.353
CURRENT FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 165
LENGTH: 1636
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020160382A1 2434655CB1
US-09-981-353-165

Alignment Scores:
Pred. No.: 0
Score: 2802.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%

Length: 1636
Matches: 527
Conservative: 0
Mismatch: 0
Indels: 0

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Db 90 GGAATCTGTGGGAAATCTCGGTGGTGGCCCTGGACATGAGCCATTGGCTTAATGTCAAG 149
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Db 330 TTATCAACCTGGCAATCAGTTATATAATTAATGATTTTCTTCAATTAAGAGCAACT 389
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Db 570 AGCTGTGGGAAACTTCACACTCCACTTCTATGTACTGTGCTATGACAGAGCTAACA 629
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Db 630 GACAGATACCTTTCTGGAAGAGTAAATAATCAATCTTTCAGTTTGTTCACCTTC 689
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QY 261 AspPheGluPheProGlnProTyrGlnProAsnPheGluPheValGlyLysLeuHisCys 280
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QY 281 LysProAlaLysAlaLeuProLysGluMetGluAsnPheValGlnSerSerGlyLysAsp 300
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QY 521 ArgLysIleGluLysArgGlu 527
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RESULT 3
US-10-052-586-521
Sequence 521, Application US/10052586
Patent No. US20020127584A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C1
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US/10/052,586
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
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; PRIOR APPLICATION NUMBER: 60/235,044
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1584
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-678-3

Alignment Scores:
Pred. No.: 0 Length: 1584
Score: 2797.00 Matches: 526
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 99.82% Indels: 0
DB: 9 Gaps: 0

US-09-784-340-2 (1-527) x US-09-962-678-3 (1-1584)

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QY 21 GlyPheCysGlyLysValLeuValTTPProCysAspMetSerHisTTPLeuAsnValLys 40
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Db 61 GGATTCGTGGGAAAGCTGGTGGTGGCTGTGACATGAGCCATTTGGCTTAATGTCAAG 120

QY 41 ValIleLeuGlnLeuLeuValLeuValArgGlyHisGlnValThrValLeuThrHisSerLys 60
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Db 121 CTCATTTCTAGAGAGCTCATAGTGAAGGCCATGAGTAACAGTATGACTCACTCAAG 180

QY 61 ProSerLeuIleAspTyrArgLysProSerAlaLeuLysPheGlnValValHisMetPro 80
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Db 181 CCTTCGTAAATTGACTACAGAGACCTTCTGCATTGAATTTGAGGTGCTCATATGCCA 240

QY 81 GlnAspArgThrGlnGluAsnGlnIlePheValAspLeuAlaLeuAsnValLeuProGly 100
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Db 241 CAGAGCAGACAGAGAAATGAATATTTGTTCAGCTCAGCTCGAATGCTTCCAGGC 300

QY 101 LeuSerThrTTPGlnSerValIleLysLeuAsnAspPhePheValGluIleArgGlyThr 120
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Db 301 TTATCAACCTGCGCAATCAGTTATATAATTAATGATTTTGTGAAATGAAGGGAAC 360

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Db 361 TTTAAAAAGATGTGAGAGCTTATCTACATCAGAGCGCTTATGAGAGAACTCAGGAA 420

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QY 161 LeuLeuAlaValProPheValLeuThrLeuArgLieserValGlyGlyAsnMetGlnArg 180
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Db 481 TTGCTTGACAGTCCCTTTGTGCTCAGACTTAGAATTTCTGAGGGGCAATAGAGGA 540

QY 181 SerCysGlyLysLeuProAlaProLeuSerTyrValProValProMetThrGlyLeuThr 200
   |||||
Db 541 AGCTGTGGAACTTCACGCTCCACTTCTCTGATGACTGTGCTCATATACAGGACTACA 600

QY 201 AspArgMetThrPheLeuGlnArgValLysAsnSerMetLeuSerValLeuPheHisPhe 220
   |||||
Db 601 GACAGAAATGACCTTCTCTGGAAGAGCTAAATAATCAATGCTTTCAGTTTGTTCACATTC 660

QY 221 TTPileGlnAspTyrAspTyrHisPheTTPGlnGluPheTyrSerLysAlaLeuGlnArg 240
   |||||
Db 661 TCGATTTCAGGATTACGACTATCATTTTGGGAGAGTTTATAGTAAGCAATTAGGAAG 720

QY 241 ProThrThrLeuLysGlnThrValGlyLysAlaGlnIleTTPLeuIleArgThrTyrTTP 260
   |||||
Db 721 CCCACTACATTTATGTGAGCTGTGGAAAGCTGAGATATGCTTAATACGAACATATTTGG 780

QY 261 AspPheGlnPheProGlnProTyrGlnProAsnPheGlnPheValGlyGlyLeuHisCys 280

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Db 781 GATTTTGAATTTCCCAACCATACACCTACTTGTGATTGTGGAGATTCACACTGT 840
   |||||
QY 281 LysProAlaLysAlaLeuProLysGlnMetGluAsnPheValGlnSerSerGlyLysP 300
   |||||
Db 841 AAACCTGCCAAAGCTTTGGCTTAAGGAAATGGAATAATTTGTCCAGATTCAGGGAAAT 900

QY 301 GlyIleValValPheSerLeuGlySerLeuPheGlnAsnValThrGlnLysAlaAsn 320
   |||||
Db 901 GGTATTGGTGTCTTCTGTGGGTGCTACTGTTTCAAAATGTTACGAAAGAAAGCTTAT 960

QY 321 IleIleAlaSerAlaLeuAlaGlnIleProGlnLysValLeuTTPArgTyrLysGlyLys 340
   |||||
Db 961 ATCATGCTTCAGCCCTTCCAGATCCACAGAAAGGTGTATGAGGATCAAAAGAAAA 1020

QY 341 LysProSerThrLeuGlnAlaAsnThrArgLeuTyrAspTTPLeuProGlnAsnAspLeu 360
   |||||
Db 1021 AAACCATCCACATTAAGACCAATACCTCGGTGTATGATGGATGATCCCGAATGATCTT 1080

QY 361 LeuGlyHisProLysThrLysAlaPheIleThrHisGlyGlyMetAsnGlyIleTyrGln 380
   |||||
Db 1081 CTGGTCATCCCAAAACCAAGCTTTATCATCATGATGGAATGATGATGATATGAA 1140

QY 381 AlaIleTyrHisGlyValProMetValGlyValProIlePheGlyAspGlnLeuAspAsn 400
   |||||
Db 1141 GCTATTACCATGGGGTCCCTATGCTGAGGAGTCCCATATTTGCTGATCAGCTTGATTAAC 1200

QY 401 IleAlaHisMetLysAlaLysGlyAlaIleValGlnIleAsnPheLysThrMetThrSer 420
   |||||
Db 1201 ATAGCTCACATGAAAGCCCAAGAGCAGCTGTGAAATTAATCTCAAACTATGACAAAC 1260

QY 421 GluAspLeuLeuArgAlaLeuArgThrValIleThrAspSerSerTyrLysGluAsnAla 440
   |||||
Db 1261 GAAGATTATAGAGGCTTTGAGACACAGTCATACCGATTCCCTTAATAAGAAATGCT 1320

QY 441 MetArgLeuSerArgIleHisHisAspGlnProValLysProLeuAspArgAlaValPhe 460
   |||||
Db 1321 ATGAGATTATCAAGAAATCCCATGATCAACCTGTAAAGCCCTTAATGACAGAGCTTTC 1380

QY 461 TTPileGlnPheValMetArgHisLysGlyAlaLysHisLeuArgSerAlaAlaHisAsp 480
   |||||
Db 1381 TGGATCAGATTGTTCATGCGCCCAAAAGAGCCAGACACTGCGATCAGCTGCCATGAC 1440

QY 481 LeuThrTTPPheGlnHisTyrSerIleAspValIleGlyPheLeuLeuThrCysValAla 500
   |||||
Db 1441 CTCACCTGTTCCAGACACTACTATATGATGATGTGGTTCCTGCTGGCCTGTGGCA 1500

QY 501 ThrAlaIlePheLeuPheThrLysCysPheLeuPheSerCysGlnLysPheAsnLysThr 520
   |||||
Db 1501 ACTGCTATATTCTTGTTCACAAAATGTTTTTATTTCCTCTGCTCAAAAATTTAATAAACT 1560

QY 521 ArgLysIleGlnLysArgGln 527
   |||||
Db 1561 AGAAAGATAGAAAAAGAGGAA 1581

RESULT 5
US-09-962-678-1
; Sequence 1, Application US/09962678
; Patent No. US20020155499A1
; GENERAL INFORMATION:
; APPLICANT: Leiby, Kevin R.
; TITLE OF INVENTION: 32624, A NOVEL HUMAN UDP-GLUCURONOSYL
; TITLE OF INVENTION: AND UDP-GLYCOSYL TRANSFERASE AND USES THEREOF
; FILE REFERENCE: 10448-094001
; CURRENT APPLICATION NUMBER: US/09/962,678
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/235,044
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3006
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (33)...(1613)
US-09-962-678-1

Alignment Scores:
Pred. No.: 0 Length: 3006
Score: 2797.00 Matches: 526
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 99.82% Indels: 0
DB: 9 Gaps: 0

US-09-784-340-2 (1-527) x US-09-962-678-1 (1-3006)

OY 1 MetarSeraSplySerAlaLeuValPheLeuLeuGlnLeuPheCysValGlyCys 20
DB 33 ATGAGGTCTGACACAGTCACTTGGTATTTGCTCTCCACACTCTTGTGTGGCTCT 92
OY 21 GlyPheCysGlyLysValLeuValTrrProCysAspMetSerHisTrrLeuAsnValLys 40
DB 93 GGATTCCTGGGAAAGTCCCTGGTGGCCCTGACATGAGCCATTGGCTTATGTCAAG 152
OY 41 ValIleLeuGlnGluLeuIleValArgGlyHisGluValTrrValLeuThrHisSerLys 60
DB 153 GTCATCTTGAAGAGCTCTACTGAGAGGCCATGAGGTACAGTATTGCTCACTCAAG 212
OY 61 ProSerLeuIleAspTrrArgLysProSerAlaLeuLysPheGluValValHisMetPro 80
DB 213 CCTGGTTCATGACTACAGAAAGCCCTTCGATTGAATTGGAGTGGCTCATATGCCA 272
OY 81 GlnAspArgThrGlnGlnAsnGluIlePheValAspLeuAlaLeuAsnValLeuProGly 100
DB 273 CAGGACAGACAGAAAGAAATATTGTTGACCTGACCTGTAATCTTGGCCAGGC 332
OY 101 LeuSerThrTrrGlnSerValIleLysLeuAsnAspPhePheValGluIleArgGlyThr 120
DB 333 TTATCACTGGCANTCACTTATATAAATTAAATGATTTTGTGTAATTAAGAGAACT 392
OY 121 LeuLysMetMetCysGluSerPheIleTrrAsnGlnTrrLeuMetLysLysLeuGlnGlu 140
DB 393 TTAATAATGATGTGTGAGAGCTTATCTCAATCAAGACCTTATGAAGAAAGCTACAGAA 452
OY 141 ThrAsnTrrAspValMetLeuIleAspProValIleProCysGlyAspLeuMetAlaGlu 160
DB 453 ACCAATCTGACGATGATAGCTTATAGACCTGTGATTCCCTGTGAGACCTGATGGCTGAG 512
OY 161 LeuLeuAlaValProPheValLeuThrLeuArgIleSerValGlyLysAsnMetGluArg 180
DB 513 TTGCTTGACAGTCCCTTTTGTCTCACACTTACAAATTTCTGTAGGAGCAATATGGAGCGA 572
OY 181 SerCysGlyLysLeuProAlaProLeuSerTrrValProValProMetThrGlyLeuThr 200
DB 573 ACCTGTGGGAAACCTCCACACTTCCTATGTACCTGCTCCATATGACAGACTAACA 632
OY 201 AspArgMetThrPheLeuGlnArgValLysAsnSerMetLeuSerValLeuPheHisPhe 220
DB 633 GACAAATATGACCTTCTTGAGAAAGAGTAAATAATTCATAGTCTTTCAGTTTGTCCACTTC 692
OY 221 TrrPileGlnAspTrrAspTrrHisPheTrrPglGluLupPheTrrSerLysAlaLeuGlyArg 240
DB 693 TGGATTCCAGATTACGACATCATTTTGGGAAAGATTTTAAAGTAGGCAATTAGGAAG 752
OY 241 ProThrThrLeuCysGluThrValGlyLysAlaGluIleTrrPheIleArgThrTrrTrr 260
DB 753 CCCACTACATATATGTAGAGACTGTGGAAAAAGCTGAGATATGCTAATATAGACATATGG 812
OY 261 AspPheGlnPheProGlnProTrrGlnProAsnPheGluPheValGlyLysLeuHisCys 280
DB 813 GATTTTGAATTTCTCAACCATATCAACACTTAACCTTGAATTTGTGGAGATTGCACTGT 872
OY 281 LysProAlaLysAlaLeuProLysGluMetGluAsnPheValGlnSerSerGlyLysAsp 300
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DB 873 AAACCTGCCAAAGCTTTGGCTTAGGAAATGGAATTTTGTCCAGAGTTCAAGGCAAGT 932
OY 301 GlyIleValAlaPheSerLeuGlySerLeuPheGlnAsnValTrrGluLysAlaAsn 320
DB 933 GGTATTTGTGCTTTTCTCTGTGGGTCACTGTTCAAAATGTTACAGAAAGAAAGCTTAT 992
OY 321 IleIleIleSerAlaLeuAlaGlnIleProGlnLysValLeuTrrPargTrrLysGlyLys 340
DB 993 ATCATTTGCTTCAGCCCTTCCAGATCCACAGAAAGGTGTTATGAGAGTCAAAAGGAAA 1052
OY 341 LysProSerThrLeuGlnValAsnThrArgLeuTrrAspTrrIleProGlnAsnAspLeu 360
DB 1053 AAACCATCCACATTTAGAGCCATATCTGGCTGTATGATTTGATACCCACAGATATCTT 1112
OY 361 LeuGlyHisProLysThrLysAlaPheIleThrHisGlyGlyMetAsnGlyIleTrrGlu 380
DB 1113 CTGGTCATCCCAAAACCAAGCTTTATCACTCATGGTGGAAATGAAATGGATCTATGAA 1172
OY 381 AlaIleTrrHisGlyValProMetValGlyValProIlePheGlyAspGlnLeuAspAsn 400
DB 1173 GGTATTTACCATGGGGTCCCTATGTGGAGATTCCCATATTTGGTATCAGCTTATATAC 1232
OY 401 IleAlaHisMetLysAlaLysGlyAlaAlaValAlaGluIleAsnPheLysThrMetThrSer 420
DB 1233 ATAGCTCACTAAGGCCCAAGAGACAGCTTGAATAATTAATTAACAACTATGCAAGC 1292
OY 421 GluAspLeuLeuArgAlaLeuArgThrValIleThrAspSerSerTrrLysGlnAsnAla 440
DB 1293 GAAGATTTCAGAGGCTTTGAGAACAGTCATTACCGATTCCTCTTATTAAGAAATGCT 1352
OY 441 MetArgLeuSerArgIleHisHisAspGlnProValLysProLeuAspArgAlaValPhe 460
DB 1353 ATGAGATTATCAAGAAATTCACCATATCAACCTGTAAACCCCTGTGATCAGCACTTTC 1412
OY 461 TrrPileGluPheValMetArgHisLysGlyAlaLysHisLeuArgSerAlaIleHisAsp 480
DB 1413 TGGATCGAGTTTGTCAATGCGCCACAAGAGGCCAAGCACTCGATCAGTCCCATGAC 1472
OY 481 LeuThrTrrPheGlnHisTrrSerIleAspValIleGlyPheLeuLeuThrCysValAla 500
DB 1473 CTCACCTGGTTCACACACTCACTATAGATGATTTGGGTCTCTGCGCTGTGGCA 1532
OY 501 ThrAlaIlePheLeuPheThrLysCysPheLeuPheSerCysGlnLysPheAsnLysThr 520
DB 1533 ACTGCTATATCTTGTTCACAAAAATGTTTATTTCTCTGTCAAAAAATTAATAAACT 1592
OY 521 ArgLysIleGluLysArgGlu 527
DB 1593 AGAAAGATTAGAAAGAGGCA 1613

RESULT 6
US-09-981-353-83
; Sequence 83, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 83
; LENGTH: 1889
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID NO. US20020160382A1 255002.4
; NAME/KEY: unsure
; LOCATION: 232, 243-244
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US-09-880-107-3292

Alignment Scores:

Pred. No.:	5,96e-195	Length:	2090
Score:	1713.00	Matches:	327
Percent Similarity:	76.09%	Conservative:	74
Best Local Similarity:	62.05%	Mismatches:	114
Query Match:	61.13%	Indels:	12
DB:	10	Gaps:	5

US-09-784-340-2 (1-527) x US-09-880-107-3292 (1-2090)

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QY 9 ValPheLeuLeuLeuLeuLeuPheCys---ValGlyCysGlyPheCysGlyLeuValLeu 27
    |||||
DB 43 GTCCTTCGCTGATACAGCTCAGTTGTTACTTACTTACGTCGGAGCGCTGGAAAGTGCTA 102
    |||||
QY 28 ValTTPProCysAspMetSerHisTTPLeuAsnValLysValLLeuLeuGluLeuLeu 47
    |||||
DB 103 GTCGCCCCACAGAAATACGCCATTCGATTAATATGAAAGCAATCCGGAAGCTTGTT 162
    |||||
QY 48 ValArgGlyHisGluValThrValLeuThrHisSerLysProSerLeuLeuAspTyrArg 67
    |||||
DB 163 CAGAGGGGATGATGAGTGCTGTTGACATCTTCGCTTACTCTTGTCAATGCGCACT 222
    |||||
QY 68 LysProSerAlaLeuLysPheGluValValHisMetProGlnAspArgThrGluGluAsn 87
    |||||
DB 223 AATCATCTCGCATTAATTAAGAGTT-----TATCCTACATCTTAACTAAATAATGAT 276
    |||||
QY 88 GluIlePheValAspLeuAlaLeuAsnValLeuPro-----GlyLeuSerThr 103
    |||||
DB 277 -----TTGGAAGATCTCTTCGAAATTCGATAGATGATATGATGCTGTTCAAAA 330
    |||||
QY 104 -----TTPGlnSerValIleLysLeuAsnAspPhePheValIleuLeuGlyThr 120
    |||||
DB 331 AATACATTTTGGCATATTTTTCACAAATTAACAAGAAATGTGTTGGAAATTAATGACTAC 390
    |||||
QY 121 LeuLysMetMetCysGlnSerPheIleTyrAsnGlnThrLeuMetLysLysLeuGlnGlu 140
    |||||
DB 391 AGTAACAACCTCTGTAACATGCAATGCAATTAAGAACTTATGATGAACACACAAAGAG 450
    |||||
QY 141 ThrAsnTyrAspValMetLeuIleAspProValIleProCysGlyAspLeuMetAlaGlu 160
    |||||
DB 451 TCAAAGTTTGATGTCATCTGCGCAGATGCCCTTAATCCCTGCTGAGCTACTGCGTGA 510
    |||||
QY 161 LeuLeuAlaValProPheValLeuThrLeuArgIleSerValGlyLysMetGluArg 180
    |||||
DB 511 CTATTTTAACATACCTCTTCTGTACAGTCTTCGATCTCTGTTGGCTACACATTTGAGAAG 570
    |||||
QY 181 SerCysGlyLysLeuProAlaProLeuSerTyrValProValProMetThrGlyLeuThr 200
    |||||
DB 571 AATGGGGAGAGATTTCTGTTCCCTCTCTCTATGACCTGTTGTTATGTCAGAAATTAAGT 630
    |||||
QY 201 AspArgMetThrPheLeuGluArgValLysAsnSerMetLeuSerValLeuPheHisPhe 220
    |||||
DB 631 GATCAAAATATTTTCTGAGAGAGATAAAAAATATGATACATATCTTATTTTGTACTTT 690
    |||||
QY 221 TTPIleGlnAspTyrAspTyrHisPheTTPGluGluPheTyrSerLysAlaLeuGlyArg 240
    |||||
DB 691 TGGTTTCAAAATTTATGATGTAAGAAATGGACACAGTTTATTAATGAAGTTCTAGAGAA 750
    |||||
QY 241 ProThrThrLeuCysGlnThrValGlyLysAlaGluIleTyrLeuIleArgThrTyrTrp 260
    |||||
DB 751 CCCACTACATTTTGTAGACATGGGAAAGCTGAATGTGCTCTTTCGAACTTATGG 810
    |||||
QY 261 AspPheGluPheProGlnProTyrGlnProAsnPheGluPheValGlyLeuHisCys 280
    |||||
DB 811 GATTTTGAATTTCTCGCCCATCTTCAAAATGTTGATTTGTTGAGAGACTTCACTGT 870
    |||||
QY 281 LysProAlaLysAlaLeuProLysGluMetGluAsnPheValGlnSerSerGlyGluAsp 300
    |||||
DB 871 AAACCAAGCCAAACCCCTGCTTAAGAAATGGAAGACTTTTGTGAGAGCTCTGGAAGAAAT 930
    |||||
QY 301 GlyIleValValPheSerLeuGlySerLeuPheGlnAsnValThrGluGluLysAlaAsn 320
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DB 931 GGTATTTGGTGTCTCTGCGGCTGATGATCAGTAACATGTCAACAAAGATGCCAAC 990
    |||||
QY 321 IleIleIleSerAlaLeuAlaGluIleProGlnLysValLeuThrArgTyrLysGlyLys 340
    |||||
DB 991 ATGATTTGATCAGCCCTTCCAGATCCCAAAAGAGTTCTATGAGATTTGATGGCAAG 1050
    |||||
QY 341 LysProSerThrLeuGlnLysAsnThrArgLeuTyrAspTyrIleProGlnAsnAspLeu 360
    |||||
DB 1051 AAGCCAAATACATTAAGTTCCAACTGATGATGATGATGATGATGATGATGATGATGAT 1110
    |||||
QY 361 LeuGlyHisProLysThrLysAlaPheIleThrHisGlyLysMetAsnGlyIleTyrGlu 380
    |||||
DB 1111 CTGGTCATCCCAAAACCAAGCTTTTATACATCAGTGGAGAACCAATGATCATATGAG 1170
    |||||
QY 381 AlaIleTyrHisGlyValProMetValGlyValProIlePheGlyAspGlnLeuAspAsn 400
    |||||
DB 1171 GCGATCTACCATGGGATCCCTGATGTTGCGCATTCCTGTTTGGGATCAACATGATTAAC 1230
    |||||
QY 401 IleAlaHisMetLysAlaLysGlyAlaAlaValGluIleAsnPheLysThrMetThrSer 420
    |||||
DB 1231 ATTGCTCATATGAAGCCAGGAGCGCCCTCAGTGTGACATCGAGCAATGTCAGT 1290
    |||||
QY 421 GluAspLeuLeuArgAlaLeuArgThrValIleThrAspSerSerTyrLysGluAsnAla 440
    |||||
DB 1291 AGAGATTTGCTCATATCATTAAGTACATTAATGACCCCTCTATTAAGAGATGTC 1350
    |||||
QY 441 MetArgLeuSerArgIleHisHisAspGlnProValLysProLeuAspArgAlaValPhe 460
    |||||
DB 1351 ATGAAATTTATCAAGATTCATCATGACCAACCAATGAAACCCCTGATGAGACAGTCTTC 1410
    |||||
QY 461 TTPIleGluPheValMetArgHisLysGlyAlaLysHisLeuArgSerAlaAlaHisAsp 480
    |||||
DB 1411 TGGATGAGTTTGTCTGCGCCACAAAGAGCCAAACACCTTCGAGTCCGACTCAACAC 1470
    |||||
QY 481 LeuThrTTPPheGlnIleTyrSerIleAspValIleGlyPheLeuLeuThrCysValAla 500
    |||||
DB 1471 CTCACCTGGATGCAGTACACACCTTTTGATGTGATAGCATTCCTGCTGCGCTGCGGCA 1530
    |||||
QY 501 ThrAlaIlePheLeuPheThrLysCysPheLeuPheSerCysGlnLysPheAsnLysThr 520
    |||||
DB 1531 ACTGATGATTTATATCATCAAAATTTTCCGTTTGTTCGAAAGCTTCCCAAAACA 1590
    |||||
QY 521 ArgLysIleGluLysArgGlu 527
    |||||
DB 1591 GGAAGAGAGAGAAAGAGAT 1611
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RESULT 8
US-09-981-353-45
; Sequence 45, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 45
; LENGTH: 2150
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 255115.4
; NAME/KEY: unsure
; LOCATION: 2087, 2089, 2094, 2096-2098, 2108, 2110, 2112, 2115-2116, 2120,
; LOCATION: 2122-2123, 2125, 2136
; OTHER INFORMATION: a, t, c, g, or other
US-09-981-353-45

815 TCGAATTTTTCAGTTTTCCTATCCACTCTTACCAATGTTGATTTCGTCAGGACTCCAC 8

OY	280	CysLysProAlaLysAlaLeuProLysGluMetGluAsnPhenValGlnSerSerGlyGlu	299
OY	280	CysLysProAlaLysAlaLeuProLysGluMetGluAsnPhenValGlnSerSerGlyGlu	299
Db	875	TGCAAACCTCCCAAAACCCCTGGCTTAAGGAATAAGAAAGACTTTGTACGACACTCTGGAGAA	934
OY	300	AspAlaGlyLeuValValPheSerLeuGlySerLeuPheGlnAsnValIrrhGluGluLysAla	319
Db	935	AATGGTGTGTGGTGTCTTCTCTCGGGGTCAATGCGTCAGTAAACATGACAGAAAGAAAGGCC	994
OY	320	AsnIleLeuLaserAlaLeuAlaGlnIleProGlnLysValLeuTTPaGlyLysGly	339
Db	995	AACCTAATTGCATCAGCCCGCCGACCAATCCCAAAAGAGTCTGTGGAGATTGTGATGGC	1054
OY	340	LysLysProSerThrLeuGlyAlaAsnThrArgLeuTyrAspTrrPileProGlnAsnAsp	359
Db	1055	AATAACCCAGATACCTTAGTTCATCTACTGGCTCTCAAGTGGATGCCCAAGAAATGAC	1114
OY	360	LeuLeuGlyHisProLysThrLysAlaPheIleThrHisGlyGlyMetAsnGlyIleLeuTyr	379
Db	1115	CTTCTAGTCTCATCCAAAGACCAAGAGCTTTTATACCAAGGAGGAGCCAAAGGCAATCTTAC	1174
OY	380	GluAlaIleTyrHisGlyValProMetValGlyValProIlePheGlyAspGlnLeuAsp	399
Db	1175	GAGGCAATCTACCATGGGATCCCTATGAGTGGGATTCATCTTTGGCTGATCAACCTGAT	1234
OY	400	AsnIleAlaHisMetLysAlaLysGlyAlaAlaValGluIleAsnPhenLysThrMetThr	419
Db	1235	AACATTCGTCACATGAAGGCCAGGAGCGAGCTGTAGAGTGGAGCTTCAACACATGTCG	1294
OY	420	SerGluAspLeuLeuArgAlaLeuArgThrValIleThrAspSerSerTyrLysGluAsn	439
Db	1295	ACTACAGACTGCTCGAATGCACTTATAAGAGCTAATTAATGATCCTTCATATAAGAGAGAT	1354
OY	440	AlaMetArgLysSerArgIleHisHisAspGlnProValLysProLeuAspArgAlaVal	459
Db	1355	GTTATGAATTTATTCAGAAATTCACATGATCAACATGACCAAGTGAAGCCCTGGATGACCACTC	1414
OY	460	PheTrrPileGluPheValMetArgHisLysGlyAlaLysHisLeuArgSerAlaIleHis	479
Db	1415	TTCGTGATTGAATTTGTCATCGCCGACCAAGAGACTTAACACCTTGGGTTGCACCCAC	1474
OY	480	AspLeuThrTrrPheGlnHisTyrSerIleAspValIleGlyPheLeuLeuThrCysVal	499
Db	1475	GACCTACCTGGTTCCAGACACACACTTTGGATGTGATTGGGTTCCCTGGCTGTGTGTG	1534
OY	500	AlaThrAlaIlePheLeuPheThrLysCysPheLeuPheSerCysGlnLysPheAsnLys	519
Db	1535	GCAACTGATATTATTCGTCTCAAAATGTTGTCTGTTTCTTCTTGGAAAGTTTGTCTAGA	1594
OY	520	ThrArgLysIleGluLysArgGlu	527
Db	1595	AAAGCAAAAGAGGAAAAAATGAT	1618
RESULT 13			
US-09-880-107-2120			
Sequence 2120, Application US/09880107			
Patent No. US20020142981A1			
GENERAL INFORMATION:			
APPLICANT: Horne, Darci T.			
APPLICANT: Vockley, Joseph G.			
APPLICANT: Scherf, Uwe			
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer			
FILE REFERENCE: 44921-5028-WO			
CURRENT APPLICATION NUMBER: US/09/880,107			
CURRENT FILING DATE: 2001-06-14			
PRIOR APPLICATION NUMBER: US 60/211,379			
PRIOR FILING DATE: 2000-06-14			
PRIOR APPLICATION NUMBER: US 60/237,054			
PRIOR FILING DATE: 2000-10-02			
NUMBER OF SEQ ID NOS: 3950			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 2120			
LENGTH: 1855			


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Query Match: 57.26% Indels: 20
DB: 9 Gaps: 4
US-09-784-340-2 (1-527) x US-09-981-353-189 (1-1712)

QY 9 ValPheLeuLeuLeuLeuPheCys---ValGlyCysGlyPheCysGlyLysValLeu 27
   ||| |||||::: ||| ||| ||| ||||| |||||
Db 38 GTTCTCTGCTGATACATCTCAGTGTACTTACCTAGCTCTGAGAGTTGTGAAAAAGTCTG 97

QY 28 ValTrrProCysAspMetSerHisTrrPheAsnValLysValLleLeuGluGluLeuIle 47
   ||||| :::: ||||| |||||::: ||| ||| ||||| |||||
Db 98 GTGTGGCCGCAAAATACACCCATGTGATGAATGAAAGCAATCCCGAAAGCGTTGTT 157

QY 48 ValArgGlyHisGluValTrrValLeuTrrHisSerLysProSerLeuIleAspTyrArg 67
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 158 CAGAGAGGTATAGGTGACTGACTGCGCATCTTCACCTTCTTTTGTGATCCCAAT 217

QY 68 LysProSerAlaLeuLysPheGluValValHisMetProGlnAspArgTrrGluAsn 87
   ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 218 GATGCATCCACTCTTAATTTGAAGTTTATCCATCTTAACTTAACGTAATTTGAG 277

QY 88 GluIlePheValAspLeuAlaLeuAsnValLeuProGlyLeuSerHisTrrGlnSerVal 107
   ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 278 AATATC-----ATCATCAACAGGTTAAGAGATGG---TCAGAC 313

QY 108 IleLysLeuAsnAspPhePheVal-----GluIle 117
   |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db 314 ATTCGAAAAGATAGCTTTTGTTATATTTTTCACAAAGACAAACAAATCCCTGGGCAATTA 373

QY 118 ArgGlyTrrLeuLysMetMetCysGlnSerPheIleTyrAsnGlnTrrLeuMetLysLys 137
   |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db 374 TATGACATATTTAGAAACTTCTTAAGATGTAGTTTCAATAAGAAATGATTAAGAAAAA 433

QY 138 LeuGluGluTrrAsnTrrAspValMetLeuIleAspProValIleProCysGlyAspLeu 157
   ||||| |||||::: ::|||::: ||| ||| ||||| |||||
Db 434 CTACAAAGATCAAGATTGTCATCGTTTTCAGATGCTGTTTCCCTGGTGAGCTG 493

QY 158 MetAlaGluLeuLeuAlaValPropheValLeuTrrLeuArgLleSerValGlyLysAsn 177
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 494 CTGGCTGCGCTACTTAACATACGTTTGTGTACAGTCTCCGCTTACTCTGCTACACA 533

QY 178 MetGluArgSerCysGlyLysLeuProAlaProLeuSerTyrValProValPrometTrr 197
   ::||| ||||| ||||| ||||| ||||| ||||| |||||
Db 554 ATTTGAAAGGCACAGTGGAGGATGTTTCCCTCTTCAATACCTATTTGTTATGTCA 613

QY 198 GlyLeuTrrAspArgMetTrrPheLeuGluArgValLysAsnSerMetLeuSerValLeu 217
   ||||| |||||::: ||||| ||||| ||||| ||||| |||||
Db 614 AATTTAAGTATCAAAATGACTTTTCATGAGAGGTAATAAATGATCTATGTGCTTTAT 673

QY 218 PheHisPheTrrPheGlnAspTrrAspTrrHisPheTrrGluGluPheTrrSerLysAla 237
   ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 674 TTTGACTTTTGGTCCAAATGTGTGATATGAGAACTGGAGATCAGTTTACAGTGAAGTT 733

QY 238 LeuGlyArgProTrrTrrLeuCysGluTrrValGlyLysAlaGluIleTrrPheLeuIleArg 257
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 734 TTAGAGAGACCCACTATATTGAGACAAATGGAAAGCTGACATATGCTTATGCGA 793

QY 258 ThrTrrTrrAspPheGluPheProGlnProTyrGlnProAsnPheGluPheValGlyGly 277
   ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 794 AACTCTGGAGTTTCAATTTCTCATCTTCATCCATTCCTGTAACCAACGTTGTTGGAGGA 853

QY 278 LeuHisCys-LysProAlaLysAlaLeuProLysGluMetGluAsnPheValGlnSer 297
   ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 854 TTCCACTGGCAAAACCTGCCAAACCTTACTTAAGGAATGGAGAGATTGTACAGAGCTC 913

QY 297 rGlyGluAspGlyLleValValPheSerLeuGlySerLeuPheGlnAsnValTrrGluGlu 317
   ||||| |||||::: ||||| ||||| ||||| ||||| |||||
Db 914 TGGAGAAATATGTTGTGTGTTTCTGCGGCTGAGTAAAGTAAACATGACAGCAGA 973

QY 317 uLysAlaAsnIleIleAlaSerAlaLeuAlaGlnIleProGlnLysValLeuTrrArgTyr 337
   ||::: ||||| ||||| ||||| ||||| ||||| |||||
Db 974 AAGGGCAATGTAAATTGCAACAGCCTTGCAAGATCCACAAAGGTTCTGTGAGATT 1033

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QY 337 rLysGlyLysLysProSerTrrPheGluAlaAsnTrrArgLeuTrrAspTrrPheProGlu 357
   : ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1034 TGACGGGAATTAACCAAGATGCCCTTAGCTCATACTCCGGCTGTACAAAGGATACCCCA 1093

QY 357 nasAspLeuLeuGlyHisProLysTrrLysAlaPheIleTrrHisGlyGlyMetAsnGlu 377
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1094 GAATGACCTTCTAGTGCATCCAAACCAAGAGCTTTATATCACTGATGAGCCCAATGG 1153

QY 377 yLleTrrGluAlaIleTrrHisGlyValPrometValGlyValProIlePheGluAspGlu 397
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1154 CATTTATGAGCAATGTACCATGGATCCCTATGAGGCGCATTCATGTGTTTTGTATCA 1213

QY 397 nLeuAspAsnIleAlaHisMetLysAlaLysGlyAlaValGluIleAsnPheLysTrr 417
   | ||||| ||||| ||||| ||||| ||||| |||||
Db 1214 ACCTGATATCATTTGCTCACAATGAAGCCCAAGAGACGCTTATAGATGTGACTTCAACAC 1273

QY 417 rMetTrrSerGluAspLeuLeuArgAlaLeuArgTrrValIleTrrAspSerSerTrrLys 437
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1274 AATGTGAGATACAGACCTGCTGAATGCACAGACAGTAAATTAATGATCCCTTATATGA 1333

QY 437 sGluAsnAlaMetArgLeuSerArgLleHisAspGlnProValLysProLeuAspArg 457
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1334 AGAGAAATATTATGAATTTCAAGAAATTCACACATGATCAACAGTAAAGCCCTGGATCG 1393

QY 457 gAlaValPheTrrPheGluPheValMetArgHisLysGlyAlaLysHisLeuArgSerAl 477
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1394 AGCAGTCTTGTGATTTGAATTTGTCAATGCCCAACAAAGAGCCAAACACCTTGAATGGC 1453

QY 477 aAlaHisAspLeuTrrTrrPheGlnHisTrrSerLleAspValIleGlyPheLeuLeuTh 497
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1454 AGCCCATGACCTCACCCTGGTCCAGTACACATCTTTGGATGTGATGGGTTCTGCTGGC 1513

QY 497 rCysValAlaThrAlaIlePheLeuPheThrLysCysPheLeuPheSerCysGlnLysPhe 517
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1514 CTGTGGGCAACCTGTATATTATTCATCACAAAGTTTGTCTGTTTGTCTGGAAGTT 1573

QY 517 eAsnLysTrrArgLysIleGluLysArgGlu 527
   |::: ||| ||||| |||||
Db 1574 TGTACAAAAGGAAAGGAAAGGAAAGAGAT 1604

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 Job time : 101 secs

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